

AREN0308.ST25.txt
SEQUENCE LISTING

<110> Chen, Ruoping
Chu, Zhi Liang
Dang, Huong T.
Lowitz, Kevin P.
Pride, Cameron

<120> Endogenous And Non-Endogenous Versions of Human G Protein-Coupled Receptors

<130> AREN-0308

<150> 09/170,496
<151> 1998-10-13

<150> PCT/US99/23938
<151> 1998-10-13

<150> 60/253,404
<151> 2000-11-27

<150> 60/255,366
<151> 2000-12-12

<150> 60/270,286
<151> 2001-02-20

<150> 60/282,365
<151> 2001-04-06

<150> 60/270,266
<151> 2001-02-20

<150> 60/282,032
<151> 2001-04-06

<150> 60/282,358
<151> 2001-04-06

<150> 60/282,356
<151> 2001-04-06

<150> 60/290,917
<151> 2001-05-14

<150> 60/309,208
<151> 2001-07-31

<160> 67

<170> PatentIn version 3.1

<210> 1
<211> 1002
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 1
atgttgagct gcagctgggt caacggcaca gggctggtgg aggagctgcc tgcctgccag 60
gacctgcagc tggggctgtc actgttgctg ctgctgggcc tgggtggtggg cgtgccagtg 120

AREN0308.ST25.txt

```

ggcctgtgct acaacgccct gctggtgctg gccaacctac acagcaaggc cagcatgacc 180
atgccggacg tgtactttgt caacatggca gtggcaggcc tgggtgctcag cgccctggcc 240
cctgtgcacc tgetcggccc cccgagctcc cgggtggcgc tgtggagtgt gggcggcgaa 300
gtccacgtgg cactgcagat ccccttcaat gtgtcctcac tggtaggcat gtactccacc 360
gccctgctga gctcgcacca ctacatcgag cgtgcactgc cgcggaccta catggccagc 420
gtgtacaaca cgcggcacgt gtgcggtctt gtgtggggtg gcgcgctgct gaccagcttc 480
tcctcgctgc tcttctacat ctgcagccat gtgtccaccc gcgcgctaga gtgcgccaag 540
atgcagaacg cagaagctgc cgacgccacg ctggtgttca tcggctacgt ggtgccagca 600
ctggccaccc tctacgcgct ggtgctactc tcccgcgtcc gcagggagga cacgcccctg 660
gaccgggaca cgggcgggct ggagccctcg gcacacaggc tgctggtggc caccgtgtgc 720
acgcagtttg ggctctggac gccacactat ctgatcctgc tggggcacac ggtcatcatc 780
tcgcgaggga agcccggtga cgcacactac ctggggctac tgcactttgt gaaggatttc 840
tccaaactcc tggccttctc cagcagcttt gtgacaccac ttctctaccg ctacatgaac 900
cagagcttcc ccagcaagct ccaacggctg atgaaaaagc tgccctgcgg ggaccggcac 960
tgctccccgg accacatggg ggtgcagcag gtgctggcgt ag 1002

```

<210> 2
 <211> 333
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 2

Met Trp Ser Cys Ser Trp Phe Asn Gly Thr Gly Leu Val Glu Glu Leu
 1 5 10 15

Pro Ala Cys Gln Asp Leu Gln Leu Gly Leu Ser Leu Leu Ser Leu Leu
 20 25 30

Gly Leu Val Val Gly Val Pro Val Gly Leu Cys Tyr Asn Ala Leu Leu
 35 40 45

Val Leu Ala Asn Leu His Ser Lys Ala Ser Met Thr Met Pro Asp Val
 50 55 60

Tyr Phe Val Asn Met Ala Val Ala Gly Leu Val Leu Ser Ala Leu Ala
 65 70 75 80

Pro Val His Leu Leu Gly Pro Pro Ser Ser Arg Trp Ala Leu Trp Ser
 85 90 95

AREN0308.ST25.txt

Val Gly Gly Glu Val His Val Ala Leu Gln Ile Pro Phe Asn Val Ser
100 105 110

Ser Leu Val Ala Met Tyr Ser Thr Ala Leu Leu Ser Leu Asp His Tyr
115 120 125

Ile Glu Arg Ala Leu Pro Arg Thr Tyr Met Ala Ser Val Tyr Asn Thr
130 135 140

Arg His Val Cys Gly Phe Val Trp Gly Gly Ala Leu Leu Thr Ser Phe
145 150 155 160

Ser Ser Leu Leu Phe Tyr Ile Cys Ser His Val Ser Thr Arg Ala Leu
165 170 175

Glu Cys Ala Lys Met Gln Asn Ala Glu Ala Ala Asp Ala Thr Leu Val
180 185 190

Phe Ile Gly Tyr Val Val Pro Ala Leu Ala Thr Leu Tyr Ala Leu Val
195 200 205

Leu Leu Ser Arg Val Arg Arg Glu Asp Thr Pro Leu Asp Arg Asp Thr
210 215 220

Gly Arg Leu Glu Pro Ser Ala His Arg Leu Leu Val Ala Thr Val Cys
225 230 235 240

Thr Gln Phe Gly Leu Trp Thr Pro His Tyr Leu Ile Leu Leu Gly His
245 250 255

Thr Val Ile Ile Ser Arg Gly Lys Pro Val Asp Ala His Tyr Leu Gly
260 265 270

Leu Leu His Phe Val Lys Asp Phe Ser Lys Leu Leu Ala Phe Ser Ser
275 280 285

Ser Phe Val Thr Pro Leu Leu Tyr Arg Tyr Met Asn Gln Ser Phe Pro
290 295 300

Ser Lys Leu Gln Arg Leu Met Lys Lys Leu Pro Cys Gly Asp Arg His
305 310 315 320

Cys Ser Pro Asp His Met Gly Val Gln Gln Val Leu Ala
325 330

<210> 3
<211> 918
<212> DNA
<213> Homo sapiens

AREN0308.ST25.txt

```

<400> 3
atgcctggcc acaatacctc caggaattcc tcttgcgatc ctatagtgac accccactta 60
atcagcctct acttcatagt gcttattggc gggctgggtg gtgtcatttc cattcttttc 120
ctcctggtga aaatgaacac cgggtcagtg accaccatgg cggtcattaa ctgggtggtg 180
gtccacagcg tttttctgct gacagtgcc a tttcgcttga cctacctcat caagaagact 240
tggatgtttg ggctgccctt ctgcaaattt gtgagtgcc a tgctgcacat ccacatgtac 300
ctcacgttcc tattctatgt ggtgatcctg gtcaccagat acctcatctt cttcaagtgc 360
aaagacaaag tgggaattcta cagaaaactg catgctgtgg ctgccagtgc tggcatgtgg 420
acgctggtga ttgtcattgt ggtacccttg gttgtctccc ggtatggaat ccatgaggaa 480
tacaatgagg agcactgttt taaatttcac aaagagcttg cttacacata tgtgaaaatc 540
atcaactata tgatagtcac ttttgtcata gccgttgctg tgattctggt ggtcttccag 600
gtcttcatca ttatgttgat ggtgcagaag ctacgccact ctttactatc ccaccaggag 660
ttctgggctc agctgaaaaa cctatttttt ataggggtca tccttgtttg tttccttccc 720
taccagttct ttaggatcta ttacttgaat gttgtgacgc attccaatgc ctgtaacagc 780
aaggttgcat tttataacga aatcttcttg agtgtaacag caattagctg ctatgatttg 840
cttctctttg tctttggggg aagccattgg ttttaagcaa agataattgg cttatggaat 900
tgtgttttgt gccgttag 918

```

```

<210> 4
<211> 305
<212> PRT
<213> Homo sapiens

```

<400> 4

```

Met Pro Gly His Asn Thr Ser Arg Asn Ser Ser Cys Asp Pro Ile Val
1          5          10          15

```

```

Thr Pro His Leu Ile Ser Leu Tyr Phe Ile Val Leu Ile Gly Gly Leu
20          25          30

```

```

Val Gly Val Ile Ser Ile Leu Phe Leu Leu Val Lys Met Asn Thr Arg
35          40          45

```

```

Ser Val Thr Thr Met Ala Val Ile Asn Leu Val Val Val His Ser Val
50          55          60

```

```

Phe Leu Leu Thr Val Pro Phe Arg Leu Thr Tyr Leu Ile Lys Lys Thr
65          70          75          80

```

```

Trp Met Phe Gly Leu Pro Phe Cys Lys Phe Val Ser Ala Met Leu His
85          90          95

```

AREN0308.ST25.txt

Ile His Met Tyr Leu Thr Phe Leu Phe Tyr Val Val Ile Leu Val Thr
100 105 110

Arg Tyr Leu Ile Phe Phe Lys Cys Lys Asp Lys Val Glu Phe Tyr Arg
115 120 125

Lys Leu His Ala Val Ala Ala Ser Ala Gly Met Trp Thr Leu Val Ile
130 135 140

Val Ile Val Val Pro Leu Val Val Ser Arg Tyr Gly Ile His Glu Glu
145 150 155 160

Tyr Asn Glu Glu His Cys Phe Lys Phe His Lys Glu Leu Ala Tyr Thr
165 170 175

Tyr Val Lys Ile Ile Asn Tyr Met Ile Val Ile Phe Val Ile Ala Val
180 185 190

Ala Val Ile Leu Leu Val Phe Gln Val Phe Ile Ile Met Leu Met Val
195 200 205

Gln Lys Leu Arg His Ser Leu Leu Ser His Gln Glu Phe Trp Ala Gln
210 215 220

Leu Lys Asn Leu Phe Phe Ile Gly Val Ile Leu Val Cys Phe Leu Pro
225 230 235 240

Tyr Gln Phe Phe Arg Ile Tyr Tyr Leu Asn Val Val Thr His Ser Asn
245 250 255

Ala Cys Asn Ser Lys Val Ala Phe Tyr Asn Glu Ile Phe Leu Ser Val
260 265 270

Thr Ala Ile Ser Cys Tyr Asp Leu Leu Leu Phe Val Phe Gly Gly Ser
275 280 285

His Trp Phe Lys Gln Lys Ile Ile Gly Leu Trp Asn Cys Val Leu Cys
290 295 300

Arg
305

<210> 5
<211> 1125
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 5

<210>	6
<211>	374
<212>	PRT
<213>	Artificial Sequence
<220>	
<223>	Novel Sequence
<400>	6

Gln Asp Ser Gly Pro Gln Ser Met Gly Leu Glu Gly Arg Glu Thr Ala
20 25 30

Ser Gln Glu Phe Glu Ser His Trp Pro Glu Ile Ala Glu Arg Ser Pro
50 55 60

AREN0308.ST25.txt

Cys Val Ala Gly Val Ile Pro Val Ile Tyr Tyr Ser Val Leu Leu Gly
65 70 75 80

Leu Gly Leu Pro Val Ser Leu Leu Thr Ala Val Ala Leu Ala Arg Leu
85 90 95

Ala Thr Arg Thr Arg Arg Pro Ser Tyr Tyr Tyr Leu Leu Ala Leu Thr
100 105 110

Ala Ser Asp Ile Ile Ile Gln Val Val Ile Val Phe Ala Gly Phe Leu
115 120 125

Leu Gln Gly Ala Val Leu Ala Arg Gln Val Pro Gln Ala Val Val Arg
130 135 140

Thr Ala Asn Ile Leu Glu Phe Ala Ala Asn His Ala Ser Val Trp Ile
145 150 155 160

Ala Ile Leu Leu Thr Val Asp Arg Tyr Thr Ala Leu Cys His Pro Leu
165 170 175

His His Arg Ala Ala Ser Ser Pro Gly Arg Thr Arg Arg Ala Ile Ala
180 185 190

Ala Val Leu Ser Ala Ala Leu Leu Thr Gly Ile Pro Phe Tyr Trp Trp
195 200 205

Leu Asp Met Trp Arg Asp Thr Asp Ser Pro Arg Thr Leu Asp Glu Val
210 215 220

Leu Lys Trp Ala His Cys Leu Thr Val Tyr Phe Ile Pro Cys Gly Val
225 230 235 240

Phe Leu Val Thr Asn Ser Ala Ile Ile His Arg Leu Arg Arg Arg Gly
245 250 255

Arg Ser Gly Leu Gln Pro Arg Val Gly Lys Ser Thr Ala Ile Leu Leu
260 265 270

Gly Ile Thr Thr Leu Phe Thr Leu Leu Trp Ala Pro Arg Val Phe Val
275 280 285

Met Leu Tyr His Met Tyr Val Ala Pro Val His Arg Asp Trp Arg Val
290 295 300

His Leu Ala Leu Asp Val Ala Asn Met Val Ala Met Leu His Thr Ala
305 310 315 320

Ala Asn Phe Gly Leu Tyr Cys Phe Val Ser Lys Thr Phe Arg Ala Thr

325

330

335

Val Arg Gln Val Ile His Asp Ala Tyr Leu Pro Cys Thr Leu Ala Ser
 340 345 350

Gln Pro Glu Gly Met Ala Ala Lys Pro Val Met Glu Pro Pro Gly Leu
 355 360 365

Pro Thr Gly Ala Glu Val
 370

<210> 7

<211> 1086

<212> DNA

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 7

atgtccactg aatgcgcgcg ggcagcgggc gacgcgccct tgcgcagcct ggagcaagcc 60
 aaccgcaccc gctttccctt cttctccgac gtcaaggcgc accaccggct ggtgctggcc 120
 gcggtggaga caaccgtgct ggtgctcatc tttgcagtgt cgctgctggg caacgtgtgc 180
 gccctggtgc tgggtggcgc cgcacgacgc cgcggcgcga ctgcctgcct ggtactcaac 240
 ctctttctgc cggaacctgct cttcatcagc gctatccctc tgggtgctggc cgtgcgctgg 300
 actgaggcct ggctgctggg ccccgttgcc tgccacctgc tcttctacgt gatgacctg 360
 agcggcagcg tcaccatcct cacgctggcc gcggtcagcc tggagcgcct ggtgtgcatc 420
 gtgcacctgc agcgcggcgt gcggggtcct gggcggcggg cgcgggcagt gctgctggcg 480
 ctcatatggg gctattcggc ggtgcgcgct ctgcctctat gcgtcttctt ccgagtcgtc 540
 ccgcaacggc tccccggcgc cgaccaggaa atttcgattt gcacactgat ttggcccacc 600
 attcctggag agatctcgtg ggatgtctct tttgttactt tgaacttctt ggtgccagga 660
 ctggtcattg tgatcagtta ctccaaaatt ttacagatca caaaggcatc aaggaagagg 720
 ctcacggtaa gcctggccta ctcgagagc caccagatcc gcgtgtccca gcaggacttc 780
 cggctcttcc gcacctctt cctcctcatg gtctccttct tcatcatgtg gagccccatc 840
 atcatcacca tcctcctcat cctgatccag aacttcaagc aagacctggt catctggccg 900
 tcctctctct tctgggtggg gcccttcaca tttgctaatt cagccctaaa ccccatcctc 960
 tacaacatga cactgtgcag gaatgagtgg aagaaaattt tttgctgctt ctggttccca 1020
 gaaaaggagg ccattttaac agacacatct gtcaaaagaa atgacttgtc gattatttct 1080
 ggctaa 1086

<210> 8

<211> 361

<213> Artificial Sequence

<223> Novel Sequence

<400> 8

Leu Glu Gln Ala Asn Arg Thr Arg Phe Pro Phe Phe Ser Asp Val Lys
20 25 30

Gly Asp His Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val
35 40 45

Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
50 55 60

Val Ala Arg Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn
65 70 75 80

Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu
85 90 95

Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His
100 105 110

Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr
115 120 125

Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln
130 135 140

Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala
145 150 155 160

Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe
165 170 175

Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser
180 185 190

Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp
195 200 205

Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
210 215 220

Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg

225 230 235 240

Leu Thr Val Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
 245 250 255

Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
 260 265 270

Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
 275 280 285

Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
 290 295 300

Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
305 310 315 320

Tyr Asn Met Thr Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys
 325 330 335

Phe Trp Phe Pro Glu Lys Gly Ala Ile Leu Thr Asp Thr Ser Val Lys
 340 345 350

Arg Asn Asp Leu Ser Ile Ile Ser Gly
 355 360

<210> 9

<211> 1038

<212> DNA

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 9

atgagcagca attcatccct gctggtggct gtgcagctgt gctacgcgaa cgtgaatggg 60

tcctgtgtga aaatccccct ctcgccggga tcccgggtga ttctgtacat agtgtttggc 120

tttggggctg tgctggctgt gtttggaac ctctgggtga tgatttcaat cctccatttc 180

aagcagctgc actctccgac caattttctc gttgcctctc tggcctgcgc tgatttcttg 240

gtgggtgtga ctgtgatgcc cttcagcatg gtcaggacgg tggagagctg ctggtatatt 300

gggaggagtt tttgtacttt ccacacctgc tgtgatgtgg cattttgtta ctcttctctc 360

tttcacttgt gcttcatctc catcgacagg tacattgcgg ttactgacct cctggtctat 420

cctaccaagt tcacgtatc tgtgtcagga atttgcacg gcgtgtcctg gatcctgccc 480

ctcatgtaca gcggtgctgt gttctacaca ggtgtctatg acgatgggct ggaggaatta 540

tctgatgccc taaactgtat aggaggttgt cagaccgttg taaatcaaaa ctgggtgttg 600

acagattttc tatccttctt tatacctacc ttattatga taattctgta tggtaacata 660

```

tttcttgtgg ctagacgaca ggcgaaaaag atagaaaata ctggtagcaa gacagaatca 720
tcctcagaga gttacaaagc cagagtggcc aggagagaga gaaaagcagc taaaaccctg 780
ggggtcacag tggtagcatt tatgatttca tggttacat atagcattga ttcattaatt 840
gatgccttta tgggctttat aaccctgcc tgtatttatg agatttgctg ttggtgtgct 900
tattataact cagccatgaa tcctttgatt tatgctttat tttacccatg gtttaggaaa 960
gcaataaaag ttattgtaac tggtcagggt ttaaagaaca gttcagcaac catgaatttg 1020
ttttctgaac atatataa 1038

```

<210> 10
 <211> 345
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 10

Met Ser Ser Asn Ser Ser Leu Leu Val Ala Val Gln Leu Cys Tyr Ala
1 5 10 15

Asn Val Asn Gly Ser Cys Val Lys Ile Pro Phe Ser Pro Gly Ser Arg
20 25 30

Val Ile Leu Tyr Ile Val Phe Gly Phe Gly Ala Val Leu Ala Val Phe
35 40 45

Gly Asn Leu Leu Val Met Ile Ser Ile Leu His Phe Lys Gln Leu His
50 55 60

Ser Pro Thr Asn Phe Leu Val Ala Ser Leu Ala Cys Ala Asp Phe Leu
65 70 75 80

Val Gly Val Thr Val Met Pro Phe Ser Met Val Arg Thr Val Glu Ser
85 90 95

Cys Trp Tyr Phe Gly Arg Ser Phe Cys Thr Phe His Thr Cys Cys Asp
100 105 110

Val Ala Phe Cys Tyr Ser Ser Leu Phe His Leu Cys Phe Ile Ser Ile
115 120 125

Asp Arg Tyr Ile Ala Val Thr Asp Pro Leu Val Tyr Pro Thr Lys Phe
130 135 140

Thr Val Ser Val Ser Gly Ile Cys Ile Ser Val Ser Trp Ile Leu Pro
145 150 155 160

AREN0308.ST25.txt

```

atggtgagat ctgctgagca ctggttggtat tttggagaag tcttctgtaa aattcacaca 300
agcaccgaca ttatgctgag ctccagcctcc attttccatt tgtctttcat ctccattgac 360
cgctactatg ctgtgtgtga tccactgaga tataaagcca agatgaatat cttgggttatt 420
tgtgtgatga tcttcattag ttggagtgtc cctgctgttt ttgcatttgg aatgatcttt 480
ctggagctaa acttcaaagg cgctgaagag atatattaca aacatgttca ctgcagagga 540
ggttgctctg tcttcttttag caaaatatct ggggtactga cctttatgac ttctttttat 600
atacctggat ctattatggt atgtgtctat tacagaatat atcttatcgc taaagaacag 660
gcaagattaa ttagtgatgc caatcagaag ctccaaattg gattggaaat gaaaaatgga 720
atttcacaaa gcaaagaaag gaaagctgtg aagacattgg ggattgtgat gggagttttc 780
ctaatatgct ggtgcccttt ctttatctgt acagtcatgg acccttttct tcactacatt 840
attccacctt ctttgaatga tgtattgatt tggtttggct actgaactc tacatttaat 900
ccaatgggtt atgcattttt ctatccttgg tttagaaaag cactgaagat gatgctgttt 960
ggtaaaattt tccaaaaaga ttcattccagg tgtaaattat ttttgggaatt gagttcatag 1020

```

<210> 12
 <211> 339
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 12

Met Met Pro Phe Cys His Asn Ile Ile Asn Ile Ser Cys Val Lys Asn
1 5 10 15

Asn Trp Ser Asn Asp Val Arg Ala Ser Leu Tyr Ser Leu Met Val Leu
20 25 30

Ile Ile Leu Thr Thr Leu Val Gly Asn Leu Ile Val Ile Val Ser Ile
35 40 45

Ser His Phe Lys Gln Leu His Thr Pro Thr Asn Trp Leu Ile His Ser
50 55 60

Met Ala Thr Val Asp Phe Leu Leu Gly Cys Leu Val Met Pro Tyr Ser
65 70 75 80

Met Val Arg Ser Ala Glu His Cys Trp Tyr Phe Gly Glu Val Phe Cys
85 90 95

Lys Ile His Thr Ser Thr Asp Ile Met Leu Ser Ser Ala Ser Ile Phe
100 105 110

His Leu Ser Phe Ile Ser Ile Asp Arg Tyr Tyr Ala Val Cys Asp Pro
115 120 125

Leu Arg Tyr Lys Ala Lys Met Asn Ile Leu Val Ile Cys Val Met Ile
130 135 140

Phe Ile Ser Trp Ser Val Pro Ala Val Phe Ala Phe Gly Met Ile Phe
145 150 155 160

Leu Glu Leu Asn Phe Lys Gly Ala Glu Glu Ile Tyr Tyr Lys His Val
165 170 175

His Cys Arg Gly Gly Cys Ser Val Phe Phe Ser Lys Ile Ser Gly Val
180 185 190

Leu Thr Phe Met Thr Ser Phe Tyr Ile Pro Gly Ser Ile Met Leu Cys
195 200 205

Val Tyr Tyr Arg Ile Tyr Leu Ile Ala Lys Glu Gln Ala Arg Leu Ile
210 215 220

Ser Asp Ala Asn Gln Lys Leu Gln Ile Gly Leu Glu Met Lys Asn Gly
225 230 235 240

Ile Ser Gln Ser Lys Glu Arg Lys Ala Val Lys Thr Leu Gly Ile Val
245 250 255

Met Gly Val Phe Leu Ile Cys Trp Cys Pro Phe Phe Ile Cys Thr Val
260 265 270

Met Asp Pro Phe Leu His Tyr Ile Ile Pro Pro Thr Leu Asn Asp Val
275 280 285

Leu Ile Trp Phe Gly Tyr Leu Asn Ser Thr Phe Asn Pro Met Val Tyr
290 295 300

Ala Phe Phe Tyr Pro Trp Phe Arg Lys Ala Leu Lys Met Met Leu Phe
305 310 315 320

Gly Lys Ile Phe Gln Lys Asp Ser Ser Arg Cys Lys Leu Phe Leu Glu
325 330 335

Leu Ser Ser

<210> 13
<211> 1029
<212> DNA
<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 13

```

atgaccagca atttttccca acctgttggtg cagctttgct atgaggatgt gaatggatct      60
tgtattgaaa ctccctattc tcctgggtcc cgggtaattc tgtacacggc gtttagcttt      120
gggtctttgc tggctgtatt tggaaatctc ttagtaatga cttctgttct tcattttaag      180
cagctgcact ctccaaccaa ttttctcatt gcctctctgg cctgtgctga cttcttggtg      240
ggtgtgactg tgatgctttt cagcatggtc aggacggtgg agagctgctg gtattttgga      300
gccaaatttt gtactcttca cagttgctgt gatgtggcat tttgttactc ttctgtcctc      360
cacttgctgt tcatctgcat cgacaggtag attgtgggta ctgatccctt ggtctatgct      420
accaagtcca ccgtgtctgt gtcgggaatt tgcatacagc tgcctggat tctgcctctc      480
acgtacagcg gtgctgtggt ctacacaggt gtcaatgatg atgggctgga ggaattagta      540
agtgtctctc actgcgtagg tggctgtcaa attattgtaa gtcaaggctg ggtgttgata      600
gattttctgt tattcttcat acctaccctt gttatgataa ttctttacag taagattttt      660
cttatagcta aacaacaagc tataaaaatt gaaactacta gtagcaaagt agaatacatc      720
tcagagagtt ataaaatcag agtggccaag agagagagga aagcagctaa aacctggggg      780
gtcacgggtac tagcatttgt tatttcatgg ttaccgtata cagttgatat attaattgat      840
gcctttatgg gcttctgac ccctgcctat atctatgaaa tttgctgttg gattgcttat      900
tataactcag ccatgaatcc tttgatttat gctctatttt atccttggtt taggaaagcc      960
ataaaaactta ttttaagtgg agatgtttta aaggctagtt catcaacat tagttttatt      1020
ttagaataa                                         1029

```

<210> 14

<211> 342

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 14

```

Met Thr Ser Asn Phe Ser Gln Pro Val Val Gln Leu Cys Tyr Glu Asp
1          5          10          15

```

```

Val Asn Gly Ser Cys Ile Glu Thr Pro Tyr Ser Pro Gly Ser Arg Val
          20          25          30

```

```

Ile Leu Tyr Thr Ala Phe Ser Phe Gly Ser Leu Leu Ala Val Phe Gly
          35          40          45

```

```

Asn Leu Leu Val Met Thr Ser Val Leu His Phe Lys Gln Leu His Ser

```

50

55

60

Pro Thr Asn Phe Leu Ile Ala Ser Leu Ala Cys Ala Asp Phe Leu Val
65 70 75 80

Gly Val Thr Val Met Leu Phe Ser Met Val Arg Thr Val Glu Ser Cys
85 90 95

Trp Tyr Phe Gly Ala Lys Phe Cys Thr Leu His Ser Cys Cys Asp Val
100 105 110

Ala Phe Cys Tyr Ser Ser Val Leu His Leu Cys Phe Ile Cys Ile Asp
115 120 125

Arg Tyr Ile Val Val Thr Asp Pro Leu Val Tyr Ala Thr Lys Phe Thr
130 135 140

Val Ser Val Ser Gly Ile Cys Ile Ser Val Ser Trp Ile Leu Pro Leu
145 150 155 160

Thr Tyr Ser Gly Ala Val Phe Tyr Thr Gly Val Asn Asp Asp Gly Leu
165 170 175

Glu Glu Leu Val Ser Ala Leu Asn Cys Val Gly Gly Cys Gln Ile Ile
180 185 190

Val Ser Gln Gly Trp Val Leu Ile Asp Phe Leu Leu Phe Phe Ile Pro
195 200 205

Thr Leu Val Met Ile Ile Leu Tyr Ser Lys Ile Phe Leu Ile Ala Lys
210 215 220

Gln Gln Ala Ile Lys Ile Glu Thr Thr Ser Ser Lys Val Glu Ser Ser
225 230 235 240

Ser Glu Ser Tyr Lys Ile Arg Val Ala Lys Arg Glu Arg Lys Ala Ala
245 250 255

Lys Thr Leu Gly Val Thr Val Leu Ala Phe Val Ile Ser Trp Leu Pro
260 265 270

Tyr Thr Val Asp Ile Leu Ile Asp Ala Phe Met Gly Phe Leu Thr Pro
275 280 285

Ala Tyr Ile Tyr Glu Ile Cys Cys Trp Ser Ala Tyr Tyr Asn Ser Ala
290 295 300

Met Asn Pro Leu Ile Tyr Ala Leu Phe Tyr Pro Trp Phe Arg Lys Ala
305 310 315 320

Ile Lys Leu Ile Leu Ser Gly Asp Val Leu Lys Ala Ser Ser Ser Thr
325 330 335

Ile Ser Leu Phe Leu Glu
340

<210> 15
<211> 1062
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 15
atggagcaca cgcacgcccc cctcgcagcc aacagctcgc tgtcttgggtg gtcccccggc 60
tcggcctgcg gcttggggttt cgtgcccgtg gtctactaca gcctcttgct gtgcctcggc 120
ttaccagcaa atatcttgac agtgatcatc ctctcccagc tggcggcaag aagacagaag 180
tcctcttaca actatctctt ggcactcgtc gctgccgaca tcttggctct ctttttcata 240
gtgtttgtgg acttctctgtt ggaagatttc atcttgaaca tgcagatgcc tcaggtcccc 300
gacaagatca tagaagtgcg ggaattctca tccatccaca cctccatagc gattactgta 360
ccgttaacca ttgacaggta tatcgtgtgc tgccacccgc tcaagtacca cacggtctca 420
taccagccc gcacccggaa agtcattgta agtggtttaca tcacctgctt cctgaccagc 480
atccccattt actggtggcc caacatctgg actgaagact acatcagcac ctctgtgcat 540
cacgtcctca tctggatcca ctgcttcacc gtctacctgg tgccctgctc catcttcttc 600
atcttgaact caatcattgt gtacaagctc aggaggaaga gcaattttcg tctccgtggc 660
tactccacgg ggaagaccac cgccatcttg ttcaccatta cctccatctt tgccacactt 720
tgggcccccc gcacatcatc gattctttac cacctctatg gggcgcccat ccagaaccgc 780
tggtgtgtgc acatcatgtc cgacattgcc aacatgctag cccttctgaa cacagccatc 840
aacttcttcc tctactgctt catcagcaag cggttccgca ccatggcagc cgccacgctc 900
aaggctttct tcaagtgcc gaagcaacct gtacagttct acaccaatca taacttttcc 960
ataacaagta gcccttgat ctcgccggca aactcacact gcatcaagat gctggtgtac 1020
cagtatgaca aaaatggaaa acctataaaa gtatccccgt ga 1062

<210> 16
<211> 353
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 16

Met Glu His Thr His Ala His Leu Ala Ala Asn Ser Ser Leu Ser Trp
1 5 10 15

Trp Ser Pro Gly Ser Ala Cys Gly Leu Gly Phe Val Pro Val Val Tyr
20 25 30

Tyr Ser Leu Leu Leu Cys Leu Gly Leu Pro Ala Asn Ile Leu Thr Val
35 40 45

Ile Ile Leu Ser Gln Leu Val Ala Arg Arg Gln Lys Ser Ser Tyr Asn
50 55 60

Tyr Leu Leu Ala Leu Ala Ala Asp Ile Leu Val Leu Phe Phe Ile
65 70 75 80

Val Phe Val Asp Phe Leu Leu Glu Asp Phe Ile Leu Asn Met Gln Met
85 90 95

Pro Gln Val Pro Asp Lys Ile Ile Glu Val Leu Glu Phe Ser Ser Ile
100 105 110

His Thr Ser Ile Trp Ile Thr Val Pro Leu Thr Ile Asp Arg Tyr Ile
115 120 125

Ala Val Cys His Pro Leu Lys Tyr His Thr Val Ser Tyr Pro Ala Arg
130 135 140

Thr Arg Lys Val Ile Val Ser Val Tyr Ile Thr Cys Phe Leu Thr Ser
145 150 155 160

Ile Pro Tyr Tyr Trp Trp Pro Asn Ile Trp Thr Glu Asp Tyr Ile Ser
165 170 175

Thr Ser Val His His Val Leu Ile Trp Ile His Cys Phe Thr Val Tyr
180 185 190

Leu Val Pro Cys Ser Ile Phe Phe Ile Leu Asn Ser Ile Ile Val Tyr
195 200 205

Lys Leu Arg Arg Lys Ser Asn Phe Arg Leu Arg Gly Tyr Ser Thr Gly
210 215 220

Lys Thr Thr Ala Ile Leu Phe Thr Ile Thr Ser Ile Phe Ala Thr Leu
225 230 235 240

Trp Ala Pro Arg Ile Ile Met Ile Leu Tyr His Leu Tyr Gly Ala Pro
245 250 255

AREN0308.ST25.txt

Ile Gln Asn Arg Trp Leu Val His Ile Met Ser Asp Ile Ala Asn Met
260 265 270

Leu Ala Leu Leu Asn Thr Ala Ile Asn Phe Phe Leu Tyr Cys Phe Ile
275 280 285

Ser Lys Arg Phe Arg Thr Met Ala Ala Ala Thr Leu Lys Ala Phe Phe
290 295 300

Lys Cys Gln Lys Gln Pro Val Gln Phe Tyr Thr Asn His Asn Phe Ser
305 310 315 320

Ile Thr Ser Ser Pro Trp Ile Ser Pro Ala Asn Ser His Cys Ile Lys
325 330 335

Met Leu Val Tyr Gln Tyr Asp Lys Asn Gly Lys Pro Ile Lys Val Ser
340 345 350

Pro

<210> 17
<211> 969
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 17
atggatccaa ccgtcccagt cttcggtaca aaactgacac caatcaacgg acgtgaggag 60
actccttgct acaatcagac cctgagcttc acggtgctga cgtgcatcat ttcccttgct 120
ggactgacag gaaacgcggt agtgctctgg ctccctgggct accgcatgag caggaacgct 180
gtctccatct acatcctcaa cctggccgca gcagacttcc tcttcctcag cttccagatt 240
atacgttcgc cattacgcct catcaatatc agccatctca tccgcaaaat cctcgtttct 300
gtgatgacct ttccctactt tacaggcctg agtatgctga gcgccatcag caccgagcgc 360
tgccctgtctg ttctgtggcc catctgggtac cgtgcccgc gccccacaca cctgtcagcg 420
gtcgtgtgtg tcctgctctg gggcctgtcc ctgctgttta gtatgctgga gtggagggtc 480
tgtgacttcc tgtttagtgg tgctgattct agttggtgtg aaacgtcaga tttcatccca 540
gtcgcgtggc tgattttttt atgtgtggtt ctctgtgttt ccagcctggt cctgctggtc 600
aggatcctct gtggatcccg gaagatgccg ctgaccaggc tgtacgtgac catcctgctc 660
acagtgtctg tcttcctcct ctgcggcctg cccttcggca ttctgggggc cctaattttac 720
aggatgcacc tgaatttgga agtcttatat tgtcatgttt atctggtttg catgtccctg 780
tcctctctaa acagtagtgc caaccccatc atttacttct tcgtgggctc ctttaggcag 840

cgtaaaata ggcagaacct gaagctgggt ctccagaggg ctctgcagga caagcctgag 900
 gtggataaag gtgaagggca gcttcctgag gaaagcctgg agctgtcggg aagcagattg 960
 gggccatga 969

<210> 18
 <211> 322
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 18

Met Asp Pro Thr Val Pro Val Phe Gly Thr Lys Leu Thr Pro Ile Asn
 1 5 10 15

Gly Arg Glu Glu Thr Pro Cys Tyr Asn Gln Thr Leu Ser Phe Thr Val
 20 25 30

Leu Thr Cys Ile Ile Ser Leu Val Gly Leu Thr Gly Asn Ala Val Val
 35 40 45

Leu Trp Leu Leu Gly Tyr Arg Met Arg Arg Asn Ala Val Ser Ile Tyr
 50 55 60

Ile Leu Asn Leu Ala Ala Ala Asp Phe Leu Phe Leu Ser Phe Gln Ile
 65 70 75 80

Ile Arg Ser Pro Leu Arg Leu Ile Asn Ile Ser His Leu Ile Arg Lys
 85 90 95

Ile Leu Val Ser Val Met Thr Phe Pro Tyr Phe Thr Gly Leu Ser Met
 100 105 110

Leu Ser Ala Ile Ser Thr Glu Arg Cys Leu Ser Val Leu Trp Pro Ile
 115 120 125

Trp Tyr Arg Cys Arg Arg Pro Thr His Leu Ser Ala Val Val Cys Val
 130 135 140

Leu Leu Trp Gly Leu Ser Leu Leu Phe Ser Met Leu Glu Trp Arg Phe
 145 150 155 160

Cys Asp Phe Leu Phe Ser Gly Ala Asp Ser Ser Trp Cys Glu Thr Ser
 165 170 175

Asp Phe Ile Pro Val Ala Trp Leu Ile Phe Leu Cys Val Val Leu Cys
 180 185 190

AREN0308.ST25.txt

Val Ser Ser Leu Val Leu Leu Val Arg Ile Leu Cys Gly Ser Arg Lys
195 200 205

Met Pro Leu Thr Arg Leu Tyr Val Thr Ile Leu Leu Thr Val Leu Val
210 215 220

Phe Leu Leu Cys Gly Leu Pro Phe Gly Ile Leu Gly Ala Leu Ile Tyr
225 230 235 240

Arg Met His Leu Asn Leu Glu Val Leu Tyr Cys His Val Tyr Leu Val
245 250 255

Cys Met Ser Leu Ser Ser Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr
260 265 270

Phe Phe Val Gly Ser Phe Arg Gln Arg Gln Asn Arg Gln Asn Leu Lys
275 280 285

Leu Val Leu Gln Arg Ala Leu Gln Asp Lys Pro Glu Val Asp Lys Gly
290 295 300

Glu Gly Gln Leu Pro Glu Glu Ser Leu Glu Leu Ser Gly Ser Arg Leu
305 310 315 320

Gly Pro

<210> 19
<211> 969
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 19
atggattcaa ccatcccagt cttgggtaca gaactgacac caatcaacgg acgtgaggag 60
actccttgct acaagcagac cctgagcttc acggggctga cgtgcatcgt ttcccttgct 120
gcgctgacag gaaacgcggt tgtgctctgg ctctgggct gccgcatgcg caggaacgct 180
gtctccatct acatcctcaa cctggctgcg gccgacttcc tcttccttag cggccacatt 240
atatgttcgc cgttacgcct catcaatatc cgccatccca tctccaaaat cctcagtctt 300
gtgatgacct ttccctactt tataggccta agcatgctga gcgccatcag caccgagcgc 360
tgccctgtcca tcctgtggcc catctgggtac cactgcccgc gcccagata cctgtcatcg 420
gtcatgtgtg tcctgctctg gccctgtcc ctgctgcgga gtatcctgga gtggatgttc 480
tgtgacttcc tgtttagtgg tgctgattct gtttggtgtg aaacgtcaga ttctattaca 540
atcgcggtggc tgggtttttt atgtgtggtt ctctgtgggt ccagcctggt cctgctggtc 600

```

aggattctct gtggatcccg gaagatgccg ctgaccaggc tgtacgtgac catcctcctc 660
acagtgtctgg tcttctctct ctgtggcctg ccctttggca ttcagtgggc cctgttttcc 720
aggatccacc tggattggaa agtcttattt tgtcatgtgc atctagtttc cattttcctg 780
tccgctctta acagcagtgc caaccccatc atttacttct tctgtgggctc ctttaggcag 840
cgtcaaaata ggcagaacct gaagctggtt ctccagaggg ctctgcagga cacgcctgag 900
gtggatgaag gtggagggtg gcttcctcag gaaaccctgg agctgtcggg aagcagattg 960
gagcagtga 969

```

```

<210> 20
<211> 322
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Novel Sequence

```

```

<400> 20

```

```

Met Asp Ser Thr Ile Pro Val Leu Gly Thr Glu Leu Thr Pro Ile Asn
1           5           10           15

```

```

Gly Arg Glu Glu Thr Pro Cys Tyr Lys Gln Thr Leu Ser Phe Thr Gly
          20           25           30

```

```

Leu Thr Cys Ile Val Ser Leu Val Ala Leu Thr Gly Asn Ala Val Val
          35           40           45

```

```

Leu Trp Leu Leu Gly Cys Arg Met Arg Arg Asn Ala Val Ser Ile Tyr
          50           55           60

```

```

Ile Leu Asn Leu Val Ala Ala Asp Phe Leu Phe Leu Ser Gly His Ile
65           70           75           80

```

```

Ile Cys Ser Pro Leu Arg Leu Ile Asn Ile Arg His Pro Ile Ser Lys
          85           90           95

```

```

Ile Leu Ser Pro Val Met Thr Phe Pro Tyr Phe Ile Gly Leu Ser Met
          100           105           110

```

```

Leu Ser Ala Ile Ser Thr Glu Arg Cys Leu Ser Ile Leu Trp Pro Ile
          115           120           125

```

```

Trp Tyr His Cys Arg Arg Pro Arg Tyr Leu Ser Ser Val Met Cys Val
          130           135           140

```

```

Leu Leu Trp Ala Leu Ser Leu Leu Arg Ser Ile Leu Glu Trp Met Phe
          145           150           155           160

```

Cys Asp Phe Leu Phe Ser Gly Ala Asp Ser Val Trp Cys Glu Thr Ser
165 170 175

Asp Phe Ile Thr Ile Ala Trp Leu Val Phe Leu Cys Val Val Leu Cys
180 185 190

Gly Ser Ser Leu Val Leu Leu Val Arg Ile Leu Cys Gly Ser Arg Lys
195 200 205

Met Pro Leu Thr Arg Leu Tyr Val Thr Ile Leu Leu Thr Val Leu Val
210 215 220

Phe Leu Leu Cys Gly Leu Pro Phe Gly Ile Gln Trp Ala Leu Phe Ser
225 230 235 240

Arg Ile His Leu Asp Trp Lys Val Leu Phe Cys His Val His Leu Val
245 250 255

Ser Ile Phe Leu Ser Ala Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr
260 265 270

Phe Phe Val Gly Ser Phe Arg Gln Arg Gln Asn Arg Gln Asn Leu Lys
275 280 285

Leu Val Leu Gln Arg Ala Leu Gln Asp Thr Pro Glu Val Asp Glu Gly
290 295 300

Gly Gly Trp Leu Pro Gln Glu Thr Leu Glu Leu Ser Gly Ser Arg Leu
305 310 315 320

Glu Gln

<210> 21
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 21
cagagctctg gtggccacct ctgtcc

26

<210> 22
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 22

ctgcgtccac cagagtcacg tctcc

25

<210> 23
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 23
 gtatgcctgg ccacaatacc tccagg

26

<210> 24
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 24
 gtttgtggct aacggcacaa aacacaattc c

31

<210> 25
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 25
 ggtaccacaa tgacaatcac cagcgtcc

28

<210> 26
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 26
 ggaacgtgag gtacatgtgg atgtgcagc

29

<210> 27
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 27
 gcagtgtagc ggtcaaccgt gagcagg

27

<210> 28
 <211> 32

<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 28
tgagcaggat ggcgatccag actgaggcgt gg

32

<210> 29
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 29
gaggtacagc tggcgatgct gacag

25

<210> 30
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 30
gtggccatga gccaccctga gctcc

25

<210> 31
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 31
ggaatgtcca ctgaatgcgc gcgg

24

<210> 32
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 32
agctcgccag gtgtgagaaa ctcgg

25

<210> 33
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

TOGETHER

<400> 33
gcgttatgag cagcaattca tccctgctgg 30

<210> 34
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 34
gtatcctgaa ctctgtctat acaactgc 28

<210> 35
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 35
ccctcaggaa tgatgccctt ttgccacaa 29

<210> 36
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 36
atccatgtgg ttggtgcatg tggttcgt 28

<210> 37
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 37
aaacaacaaa cagcagaacc atgaccagc 29

<210> 38
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 38
acatagagac aagtgacatg tgtgaaccac 30

<210> 39
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 39
ggtatgagac cgtgtggtac ttgagc

26

<210> 40
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 40
gtggcagaca gcgatatacc tgtcaatgg

29

<210> 41
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 41
gcgctcatgg agcacacgca cgccac

27

<210> 42
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 42
gaggcagtag ttgccacacc tatgg

25

<210> 43
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 43
catctggttt gtgttcccag gggcaccag

29

<210> 44
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
 <223> Novel Sequence
 <400> 44
 gacagtgttg ctctcaaagt cccgtctgac tg

32

<210> 45
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Novel Sequence
 <400> 45
 ctgtttccag ggtcatcaga ctggg

25

<210> 46
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Novel Sequence
 <400> 46
 gcagcattgc tctcaaagtc ctgtctg

27

<210> 47
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence
 <400> 47
 Thr Leu Glu Ser Ile Met
 1 5

<210> 48
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence
 <400> 48
 Glu Tyr Asn Leu Val
 1 5

<210> 49
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 49

Asp Cys Gly Leu Phe
1 5

<210> 50

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 50

gatcaagctt ccatggcgtg ctgcctgagc gagg 34

<210> 51

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 51

gatcggatcc ttagaacagg ccgcagtcct tcagggttcag ctgcaggatg gtg 53

<210> 52

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 52

gtcctcactg gtggccatgt actcc 25

<210> 53

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 53

ctgcgtccac cagagtcacg tctcc 25

<210> 54

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 54

<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 60
cttcttctcc gacgtcaagg

20

<210> 61
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 61
caacggtctg acaacctcct

20

<210> 62
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 62
ttgctgtgat gtggcatttt g

21

<210> 63
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 63
caggaagccc ataaaggcat caa

23

<210> 64
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 64
acatcacctg cttcctgacc

20

<210> 65
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 65
ccagcatctt gatgcagtgt 20

<210> 66
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 66
ccatctccaa aatcctcagt c 21

<210> 67
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 67
gctgttaaga gcggacagga aa 22